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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: June 18, 2003, 15:04:29 ; Search time 15.3958 Seconds  
(without alignments)  
2160.495 Million cell updates/sec

Title: US-09-807-933B-11  
Perfect score: 1895  
Sequence: 1 MKFSIIASALLLAASSTYAA.....TFKAVTCPAEIIIAKTGCERK 346

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	672.5	35.5	229	JC7308	cellulase (EC 3.2.1.4)
2	528.5	27.9	511	S10527	endoglucanase B precursor
3	461.5	24.4	393	S59499	cellulase egII - s
4	223	11.8	1832	T31113	mucin-like glycoprotein
5	220.5	11.6	662	A45155	mucin FIM-C.1 - Af
6	208	11.0	327	S20074	promastigote surfa
7	206.5	10.9	371	S20075	larval glue protei
8	202.5	10.7	232	A60095	cellulose 1,4-beta
9	200.5	10.6	471	A26160	cellulose 1,4-beta
10	200.5	10.6	471	A38979	cellulose 1,4-beta
11	199.5	10.5	410	S68153	cellulase (EC 3.2.1.4)
12	192.5	10.2	438	S70602	cellulose 1,4-beta
13	190.5	10.1	770	T22808	hypothetical prote
14	187	9.9	307	GSF23	salivary glue prot
15	187	9.9	866	T45462	membrane glycoprot
16	187	9.9	867	T45463	membrane glycoprot
17	181.5	9.6	217	S01358	salivary glue prot
18	181.5	9.6	263	S01360	salivary glue prot
19	181.5	9.6	795	T20609	hypothetical prote
20	180	9.5	797	VGBEX1	glycoprotein X pre
21	177.5	9.4	418	S28372	cellulase (EC 3.2.1.4)
22	175.5	9.3	851	T22696	hypothetical prote
23	173	9.1	623	T75523	osteoblast specifi
24	170.5	9.0	1235	T13710	protein-tyrosine k
25	167	8.8	339	T25562	hypothetical prote
26	166.5	8.8	856	T20049	Avicelase III - As
27	166	8.8	750	T42614	probable envelope
28	166	8.8	927	T24031	hypothetical prote
29	165	8.7	354	T46740	microfilariar shea

30	164.5	8.7	790	2	T34293	hypothetical prote
31	164	8.7	3020	2	A43932	mucin 2 precursor,
32	163.5	8.6	651	2	T21175	hypothetical prote
33	163	8.6	1161	2	S57180	probable membrane
34	162.5	8.6	400	1	A28172	spasmolysin precu
35	162.5	8.6	802	2	A36910	xylanase, beta(1,3
36	162	8.5	796	2	T21460	hypothetical prote
37	161	8.5	389	2	T33340	hypothetical prote
38	161	8.5	708	2	T19474	hypothetical prote
39	160.5	8.5	388	1	JC5461	cellulase (EC 3.2.1.4)
40	158.5	8.4	2225	2	T26063	hypothetical prote
41	158	8.3	645	2	T29818	hypothetical prote
42	157.5	8.3	798	2	T34248	hypothetical prote
43	156.5	8.3	388	1	S43920	cellulase (EC 3.2.1.4)
44	156.5	8.3	693	2	T19551	mucin-like protein
45	154.5	8.2	592	2	T34446	hypothetical prote

ALIGNMENTS

RESULT 1

JC7308  
cellulase (EC 3.2.1.4) - Scopulariopsis brevicaulis  
N;Alternate names: endoglucanase I  
C;Species: Scopulariopsis brevicaulis  
C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C;Accession: JC7308; PC7087  
R;Nakatani, F.; Kawaguchi, T.; Takada, G.; Sumitani, J.; Moriyama, Y.; Arai, M.  
Biosci. Biotechnol. 64, 1238-1246, 2000  
A;Title: Cloning and sequencing of an endoglucanase gene from Scopulariopsis brevicaulis  
A;Reference number: JC7308  
A;Accession: JC7308  
A;Molecule type: DNA  
A;Residues: 1-229 <NAK>  
A;Experimental source: strain TOF-1212  
A;Accession: PC7087  
A;Molecule type: protein  
A;Residues: 21-37;149-164 <NA2>  
C;Genetics:  
A;Gene: egi  
A;Introns: 147/3  
C;Keywords: glycosidase; hydrolase

Query Match	35.5%	Score	672.5	DB	2	Length	229
Best Local Similarity	54.0%	Pred. No.	1.8e-39				
Matches	115	Conservative	33	Mismatches	62	Indels	3
Gaps	3						
QY	136	PISGFGSGNGRTTRYWDCCKPSCAWDGKASVTK-PVLTC-AKDGVSRLGSDVSGC-VGG	192				
Db	16	PAASQASCTGTTTRYWDCCKPSCSWDPKAPLSQGPMTCDINDNPLDDGGLTSGCEPGG	75				
QY	193	QAYMCNDKQFVNDVNDLAYGFAAASLGSAGASAFCCGCVELTPTNTAVAGKKFVQVNT	252				
Db	76	GAYMCSHSPWAVDDLAYGAAVNIIGGOTSDWCACYLEFTTGAVSGKGMIVQATNT	135				
QY	253	GDDLSTNHFDLQMPGGVGVGNGCQSQWNTDNGWARGYGGISISECDKLPQLOAGCK	312				
Db	136	GGDLGNHFDIAMPGGVGVGNGCTQWGSPPNGWDRYGGVHTRADCDSPFPAKAGCE	195				
QY	313	WRFGEFKNADNPVTFKAVTCPAEIIIAKTGCER	345				
Db	196	WRFDFGGTDNPDVSVREVECPAELVQKSQQR	228				

RESULT 2

S10527  
endoglucanase B precursor - Pseudomonas fluorescens  
C;Species: Pseudomonas fluorescens  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 08-Oct-1999  
C;Accession: S10527  
R;Gilbert, H.J.; Hall, J.; Hazlewood, G.P.; Ferreira, L.M.A.  
Mol. Microbiol. 4, 759-767, 1990







S70602

cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - cultivated mushroom  
N;Alternate names: cellulase  
C;Species: Agaricus bisporus (cultivated mushroom)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C;Accession: S70602  
R;Yaguchi, E.; Chow, C.M.; Challen, M.P.; Thurston, C.P.  
Curr. Genet. 30, 56-61, 1996  
A;Title: Correlation of exons with functional domains and folding regions in a cellulase  
A;Reference number: S70602; MUID:96269930; PMID:8662210  
A;Accession: S70602  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-438 <YAG>  
A;Cross-references: EMBL:Z34007; NID:g1494969; PIDN:CAA83971.1; PID:g1494970  
C;Genetics:

A;Introns: 34/1; 56/2; 96/3; 202/1; 325/3; 410/2  
C;Superfamily: cellulose 1,4-beta-cellobiosidase II; fungal cellulose-binding domain hom  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;25-56/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 10.2%; Score 192.5; DB 1; Length 438;  
Best Local Similarity 29.9%; Pred. No. 4.1e-06;  
Matches 61; Conservative 26; Mismatches 84; Indels 33; Gaps 8;  
QY 9 ALLLAASST---YAAECGQGYGCGGKMTGPTCTCTSGFTCVGAENNEWYSQCIPNDQVQ 65  
DB 5 AALLALASLVPGFVQAGSPWVGCGGNGWTGPTTCASGTCV--KQNDFFYSQCLPNNQA- 61  
QY 66 GNPKTTTT--TTKAATTTKAPVTTTKA-----TTTTTKAP-----VTTTKATTTTTTK 113  
DB 62 --PESITTPGTTTPPATTTTSGGTSGAGNPYTGKTVLSPFYADEVAQAADISNPISL 119  
QY 114 TTTKTTTTKAATTTSSNTGYSPISGFGSGNGRTTRW-----DCKPSCAWDG 162  
DB 120 ATKAASVAKIPTFWFDTVAKVPLDGLGYLADRSKNQLVOIVYDLPDRDCA--ALASNG 177  
QY 163 KASVTKPVLTCADGVSRLGSDVQ 186  
DB 178 EFLSLANDGLNKYKYNVDQIAAQIK 201

RESULT 13

T22808  
hypothetical protein F56H9.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T22808  
R;Burton, J.  
submitted to the EMBL Data Library, June 1996  
A;Reference number: Z19618  
A;Accession: T22808  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-770 <WIL>  
A;Cross-references: EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F56H9.1  
A;Experimental source: clone F56H9  
C;Genetics:  
A;Gene: CRSP:F56H9.1  
A;Map position: 5  
A;Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2

Query Match 10.1%; Score 190.5; DB 2; Length 770;  
Best Local Similarity 33.5%; Pred. No. 9.7e-06;  
Matches 61; Conservative 12; Mismatches 54; Indels 55; Gaps 9;  
QY 30 GGNK---WTGPTC--CTSGFTCVGAENNEWYS-----QCIPNDQVQGNP 68  
DB 503 GGKLIYTWKLTIFRFLSNFKCV---MKWISTLLHLLITYKLDVINSIATSP-ADP 557  
QY 69 KTTT-----TTTKAATTTKAPV-----TTTKATTTTTKAPVTTTKAT----- 107  
DB 558 TTTTTEATTTTEITTTTTEVTTTTPVTTTTTTTSTTTTSTTTTPTTTTTTTTTTPTS 617

QY 108 TTTTTKTTTTKTTTAAATTTSSNTGYSPISGFGSGNGRTTRWDCCKPSCAWDGKASVT 167  
DB 618 TTTTSTTTTPTTTTSTTTTSTTTTATPTT-----TTTTMPFCNPNVSLGMDAN 669  
QY 168 KP 169  
DB 670 NP 671

RESULT 14

GSFF3  
salivary glue protein sgs-3 - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 16-Jul-1999  
C;Accession: A03329  
R;Garfinkel, M.D.; Pruitt, R.E.; Meyerowitz, E.M.  
J. Mol. Biol. 168, 765-789, 1983  
A;Title: DNA sequences, gene regulation and modular protein evolution in the Drosophila  
A;Reference number: A92904; MUID:83294545; PMID:6411930  
A;Accession: A03329  
A;Molecule type: DNA  
A;Residues: 1-307 <GAR>  
A;Cross-references: GB:X01918; NID:g8581; PIDN:CAA25994.1; PID:g603989  
C;Comment: This protein is produced by third-instar larvae.  
C;Genetics:  
A;Gene: sgs-3  
A;Cross-references: FlyBase:FBgn0003373  
A;Map position: 3L (68C)  
A;Introns: 10/1  
C;Superfamily: salivary glue protein  
C;Keywords: salivary gland; tandem repeat

Query Match 9.9%; Score 187; DB 1; Length 307;  
Best Local Similarity 35.5%; Pred. No. 6.9e-06;  
Matches 66; Conservative 17; Mismatches 59; Indels 44; Gaps 11;

QY 1 MKFSI---IASALLLAASSTYAAECGQGYGCGGKMTGPTCTCTSGFTCVGAENNEWYSQ 57  
DB 1 MKLTATATLASILLIGSAN--VANCC-----DCG-----CPTTTTCA----- 36  
QY 58 CIPNDQVQGNPKTTTTTTTKAA-----TTTKAPVTTTKATTTT--TTTKAPVTTTKATTTT 110  
DB 37 --PRTQPPCTTTTTTTTTTTCAPPTQOSTTQPCTTSKPTTKQTTLQPLCTTPTTTKAT 94  
QY 111 TTK-TTTTKTTTKAAT--TTSSNTGYSPISGFGSGNGRTTRWDCCKPSCAWDGKASV 166  
DB 95 TTKPTTTTKATTTTKATTTTKQTTLQPLCTTP-TTTKQTTLQPLCTTPTTT---KPTT 150  
QY 167 TKPVL 172  
DB 151 TKPTT 156

RESULT 15

T45462  
membrane glycoprotein [imported] - equine herpesvirus 1  
C;Species: equine herpesvirus 1  
C;Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 09-Jun-2000  
C;Accession: T45462  
R;Kirisawa, R.; Kobayashi, T.; Kawakami, Y.; Iwai, H.  
J. Equine Sci. 7, 79-87, 1996  
A;Title: Nucleotide sequences of open reading frames 1, 24 and 71 of an attenuated equine  
A;Reference number: Z22973  
A;Accession: T45462  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-866 <KIR>  
A;Cross-references: EMBL:D88733; PIDN:BAA20037.1  
A;Experimental source: strain HH1  
C;Genetics:  
A;Note: ORF71  
C;Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein hom

us-09-807-933b-11.rpr

Wed Jun 18 17:55:06 2003

F;558-866/Domain: equine herpesvirus 1 glycoprotein homology <EHG>

Query Match 9.9%; Score 187; DB 2; Length 866;  
 Best Local Similarity 48.6%; Pred. No. 1.9e-05;  
 Matches 52; Conservative 7; Mismatches 38; Indels 10; Gaps 4;  
 Qy 70 TTTTITTKAAATTKAPVTTTKATTTTITTKAPVTTTKATTT--TTTKTTTITTKAAATTT 127  
 Db 267 TTTAAATTTAATTTAA--TTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTT 324  
 Qy 128 SSSNIGYSPISGFGSGNGRTRWDCKPSCANDGKASVTKPVLTC A 174  
 Db 325 AATTG-SPTSGSTSTTGAST-----STPSASTATSAITPTSTTSAA 365

Search completed: June 18, 2003, 17:16:21  
 Job time : 17.3958 secs